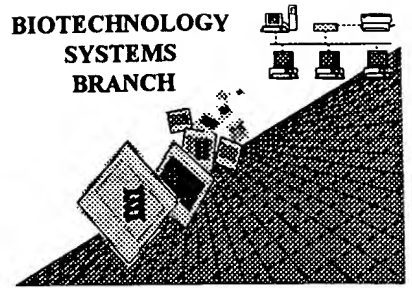


LiLee

# **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/147,405  
Art Unit / Team No. : 1645  
Date Processed by STIC: 11/15/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/147,405

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Us of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Us of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Li Lee

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/147,405

DATE: 11/15/1999  
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Input Set: I147405.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Guss, Bengt  
2 Nilsson, Martin  
3 Frykberg, Lars  
4 Flock, Jan-Ingmar  
5 Lindberg, Martin  
6 <120> TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
7 Coagulase-Negative Staphylococcus  
8 <130> FILE REFERENCE: guss 09/147405  
9 <140> CURRENT APPLICATION NUMBER: US/09/147,405  
10 <141> CURRENT FILING DATE: 1998-04-01  
11 <150> EARLIER APPLICATION NUMBER: PCT/SE97/10191  
12 <151> EARLIER FILING DATE: 1997-06-18  
13 <150> EARLIER APPLICATION NUMBER: SE 9602496-3  
14 <151> EARLIER FILING DATE: 1996-06-20  
15 <160> NUMBER OF SEQ ID NOS: 15  
16 <170> SOFTWARE: PatentIn Ver. 2.0  
17 <210> SEQ ID NO 1  
18 <211> LENGTH: 20  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Artificial Sequence  
21 <220> FEATURE:  
22 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
23 <400> SEQUENCE: 1  
24 caacaaccat ctcacacaac 20  
25 <210> SEQ ID NO 2  
26 <211> LENGTH: 22  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
31 <400> SEQUENCE: 2  
32 catcaaattg atatttccca tc 22  
33 <210> SEQ ID NO 3  
34 <211> LENGTH: 18  
35 <212> TYPE: DNA  
36 <213> ORGANISM: Staphylococcus epidermidis  
37 <400> SEQUENCE: 3  
38 gantcngant cnganagn 18  
39 <210> SEQ ID NO 4  
40 <211> LENGTH: 19  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Artificial Sequence  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

W-->

0000 see item 10 on Error Summary Sheet

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/147,405

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45 <400> SEQUENCE: 4
46     aggtcaagga caaggtgac                                19
47 <210> SEQ ID NO 5
48 <211> LENGTH: 21
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
53 <400> SEQUENCE: 5
54     ccgatgaaaa tggaaagtat c                                21
55 <210> SEQ ID NO 6
56 <211> LENGTH: 21
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
61 <400> SEQUENCE: 6
62     tccgttatct atactaaagt c                                21
63 <210> SEQ ID NO 7
64 <211> LENGTH: 21
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
69 <400> SEQUENCE: 7
70     actgatcatg atgactttag t                                21
71 <210> SEQ ID NO 8
72 <211> LENGTH: 32
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
77 <400> SEQUENCE: 8
78     gcggatccaa tcagtcaata aacaccgacg at                    32
79 <210> SEQ ID NO 9
80 <211> LENGTH: 32
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
85 <400> SEQUENCE: 9
86     cggaattctg ttcggactga tttggaagtt cc                    32
87 <210> SEQ ID NO 10
88 <211> LENGTH: 1781
89 <212> TYPE: DNA
90 <213> ORGANISM: Staphylococcus epidermidis
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (3)..(1781)
94 <400> SEQUENCE: 10

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RAW SEQUENCE LISTING  
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|     |   |     |
|-----|---|-----|
| 95  | ac cac cac cac cac cac cac ccc tct agt gat gaa gaa aag aat gat  | 47  |
| 96  | His His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp     |     |
| 97  | 1 5 10 15   |     |
| 98  | gtg atc aat aat aat cag tca ata aac acc gac gat aat aac caa ata | 95  |
| 99  | Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile |     |
| 100 | 20 25 30  |     |
| 101 | att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca | 143 |
| 102 | Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser |     |
| 103 | 35 40 45  |     |
| 104 | gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca | 191 |
| 105 | Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr |     |
| 106 | 50 55 60  |     |
| 107 | ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag | 239 |
| 108 | Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu |     |
| 109 | 65 70 75  |     |
| 110 | gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act | 287 |
| 111 | Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr |     |
| 112 | 80 85 90 95   |     |
| 113 | gcc caa caa cca tct cac aca aca ata aat aga gaa gaa tct gtt caa | 335 |
| 114 | Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln |     |
| 115 | 100 105 110   |     |
| 116 | aca agt gat aat gta gaa gat tca cac gta tca gat ttt gct aac tct | 383 |
| 117 | Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser |     |
| 118 | 115 120 125   |     |
| 119 | aaa ata aaa gag agt aac act gaa tct ggt aaa gaa gag aat act ata | 431 |
| 120 | Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile |     |
| 121 | 130 135 140   |     |
| 122 | gag caa cct aat aaa gta aaa gaa gat tca aca aca agt cag ccg tct | 479 |
| 123 | Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser |     |
| 124 | 145 150 155   |     |
| 125 | ggc tat aca aat ata gat gaa aaa att tca aat caa gat gag tta tta | 527 |
| 126 | Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu |     |
| 127 | 160 165 170 175   |     |
| 128 | aat tta cca ata aat gaa tat gaa aat aag gct aga cca tta tct aca | 575 |
| 129 | Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr |     |
| 130 | 180 185 190   |     |
| 131 | aca tct gcc caa cca tcg att aaa cgt gta acc gta aat caa tta gcg | 623 |
| 132 | Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala |     |
| 133 | 195 200 205   |     |
| 134 | gcg gaa caa ggt tcg aat gtt aac cat tta att aaa gtt act gat caa | 671 |
| 135 | Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln |     |
| 136 | 210 215 220   |     |
| 137 | agt att act gaa gga tat gat gat agt gaa ggt gtt att aaa gca cat | 719 |
| 138 | Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His |     |
| 139 | 225 230 235   |     |
| 140 | gat gct gaa aac tta atc tat gat gta act ttt gaa gta gat gat aag | 767 |
| 141 | Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys |     |
| 142 | 240 245 250 255   |     |
| 143 | gtg aaa tct ggt gat acg atg aca gtg gat ata gat aag aat aca gtt | 815 |
| 144 | Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val |     |

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|     |   |     |  |     |  |     |      |
|-----|---|-----|--|-----|--|-----|------|
| 145 |   | 260 |  | 265 |  | 270 |      |
| 146 | cca tca gat tta acc gat agc ttt aca ata cca aaa ata aaa gat aat |     |  |     |  |     | 863  |
| 147 | Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn |     |  |     |  |     |      |
| 148 |   | 275 |  | 280 |  | 285 |      |
| 149 | tct gga gaa atc atc gct aca ggt act tat gat aac aaa aat aaa caa |     |  |     |  |     | 911  |
| 150 | Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln |     |  |     |  |     |      |
| 151 |   | 290 |  | 295 |  | 300 |      |
| 152 | atc acc tat act ttt aca gat tat gta gat aag tat gaa aat att aaa |     |  |     |  |     | 959  |
| 153 | Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys |     |  |     |  |     |      |
| 154 |   | 305 |  | 310 |  | 315 |      |
| 155 | gca cac ctt aaa tta acg tca tac att gat aaa tca aag gtt cca aat |     |  |     |  |     | 1007 |
| 156 | Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn |     |  |     |  |     |      |
| 157 |   | 320 |  | 325 |  | 330 | 335  |
| 158 | aat aat acc aag tta gat gta gaa tat aaa acg gcc ctt tca tca gta |     |  |     |  |     | 1055 |
| 159 | Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val |     |  |     |  |     |      |
| 160 |   | 340 |  | 345 |  | 350 |      |
| 161 | aat aaa aca att acg gtt gaa tat caa aga cct aac gaa aat cgg act |     |  |     |  |     | 1103 |
| 162 | Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr |     |  |     |  |     |      |
| 163 |   | 355 |  | 360 |  | 365 |      |
| 164 | gct aac ctt caa agt atg ttt aca aat ata gat acg aaa aat cat aca |     |  |     |  |     | 1151 |
| 165 | Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr |     |  |     |  |     |      |
| 166 |   | 370 |  | 375 |  | 380 |      |
| 167 | gtt gag caa acg att tat att aac cct ctt cgt tat tca gcc aag gaa |     |  |     |  |     | 1199 |
| 168 | Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu |     |  |     |  |     |      |
| 169 |   | 385 |  | 390 |  | 395 |      |
| 170 | aca aat gta aat att tca ggg aat ggt gat gaa ggt tca aca att ata |     |  |     |  |     | 1247 |
| 171 | Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile |     |  |     |  |     |      |
| 172 |   | 400 |  | 405 |  | 410 | 415  |
| 173 | gac gat agc aca ata att aaa gtt tat aag gtt gga gat aat caa aat |     |  |     |  |     | 1295 |
| 174 | Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn |     |  |     |  |     |      |
| 175 |   | 420 |  | 425 |  | 430 |      |
| 176 | tta cca gat agt aac aga att tat gat tac agt gaa tat gaa gat gtc |     |  |     |  |     | 1343 |
| 177 | Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val |     |  |     |  |     |      |
| 178 |   | 435 |  | 440 |  | 445 |      |
| 179 | aca aat gat gat tat gcc caa tta gga aat aat aat gat gtg aat att |     |  |     |  |     | 1391 |
| 180 | Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile |     |  |     |  |     |      |
| 181 |   | 450 |  | 455 |  | 460 |      |
| 182 | aat ttt ggt aat ata gat tca cca tat att att aaa gtt att agt aaa |     |  |     |  |     | 1439 |
| 183 | Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys |     |  |     |  |     |      |
| 184 |   | 465 |  | 470 |  | 475 |      |
| 185 | tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca |     |  |     |  |     | 1487 |
| 186 | Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr |     |  |     |  |     |      |
| 187 |   | 480 |  | 485 |  | 490 | 495  |
| 188 | atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc |     |  |     |  |     | 1535 |
| 189 | Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser |     |  |     |  |     |      |
| 190 |   | 500 |  | 505 |  | 510 |      |
| 191 | tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt |     |  |     |  |     | 1583 |
| 192 | Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly |     |  |     |  |     |      |
| 193 |   | 515 |  | 520 |  | 525 |      |
| 194 | gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa |     |  |     |  |     | 1631 |

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DATE: 11/15/1999  
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Input Set: I147405.RAW

```

195      Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu
196              530                      535                      540
197      gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg      1679
198      Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro
199              545                      550                      555
200      ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa      1727
201      Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys
202      560                      565                      570                      575
203      tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag      1775
204      Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln
205              580                      585                      590
206      gtc gac
207      Val Asp
208      <210> SEQ ID NO 11
209      <211> LENGTH: 593
210      <212> TYPE: PRT
211      <213> ORGANISM: Staphylococcus epidermidis
212      <400> SEQUENCE: 11
213      His His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp Val
214              1                      5                      10                      15
215      Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile
216              20                      25                      30
217      Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu
218              35                      40                      45
219      Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe
220              50                      55                      60
221      Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val
222              65                      70                      75                      80
223      Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala
224              85                      90                      95
225      Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr
226              100                      105                      110
227      Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys
228              115                      120                      125
229      Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu
230              130                      135                      140
231      Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly
232              145                      150                      155                      160
233      Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn
234              165                      170                      175
235      Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr
236              180                      185                      190
237      Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala
238              195                      200                      205
239      Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser
240              210                      215                      220
241      Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp
242              225                      230                      235                      240
243      Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val
244              245                      250                      255

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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/147,405DATE: 11/15/1999  
TIME: 10:51:16

Input Set: I147405.RAW

Line ? Error/Warning

Original Text

-----  
38 W "N" or "Xaa" used: Feature required-----  
gantcngant cnganagn